

## INFORMAL SEQUENCE LISTING

SEQ ID NOs: 9598-9600 and SEQ ID NO:9611 correspond to SEQ ID NOs: 1-3 and SEQ ID NO:14 of co-pending USSN \_\_\_\_\_, filed November 6, 2001, entitled **COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY OF HEMATOLOGICAL MALIGNANCIES**, Attorney Docket No. 014058-013520US. The SEQ ID NOs. of this co-pending application USSN \_\_\_\_\_, filed November 6, 2001, entitled **COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY OF HEMATOLOGICAL MALIGNANCIES**, Attorney Docket No. 014058-013520US, will be renumbered in a subsequent amendment as SEQ ID NOs: 9598- 10,466. For clarity, the SEQ ID NOs. in this continuation-in-part of USSN \_\_\_\_\_, filed November 6, 2001, entitled **COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY OF HEMATOLOGICAL MALIGNANCIES**, Attorney Docket No. 014058-013520US. are numbered sequentially starting with SEQ ID NO:10,467.

### SEQ ID NO:9598

### LS 1384258.1 622 bp fragment of alternatively spliced variant of SEQ ID NO: 9600

INFORMATION FOR SEQ ID NO:9598:

(a) SEQUENCE CHARACTERISTICS:

<212> DNA  
<213> Homo sapiens

(b) SEQUENCE DESCRIPTION: SEQ ID NO:9598:

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gcacacaaat tgacttatta gaaggcaatg tagcatcagg aaaagtagat gtgaatgaac 60
agagtgggtca gaggagaagt tgtatttggt tgaaccttga aattaaaaat gatagaggaa 120
ttattattgg gaccgttggt aggaataatg acttttccac tgcaagactg aagatatcag 180
tgccccctcta tattctgtgc aaaagggtgct tttgactcat ccaaaaaatt gaacagtttc 240
ctgtctcatg gagatctatc acaaagtctt taaatattac tacccatgaa attggccagg 300
gttaggacat tcaaatgtct ttatccacat tccatgaagg taattgttat agattcccta 360
cctccatagg aatgcttata atggattatc tatacaatct ccacattccc acattttgca 420
ttagagaatg gaatcagtca aacctgttcc ccagagtttc ccttagagtt ctcacctgtt 480
gtcttatatc catctaggaa tccccatctc taatgtaagc ttggagatcc gggcccccg 540
gggacaggtg actgaaggac aaaaactgat cctgctctgc tcagtggctg aggggtacagg 600
aaatgtcaca ttctcctggt ac 622
```

**SEQ ID NO:9599**

**"Ly1448" 523 bp cDNA fragment of alternatively spliced variant of SEQ ID NO: 9600**

INFORMATION FOR SEQ ID NO:9599:

(a) SEQUENCE CHARACTERISTICS:

<212> DNA

<213> Homo sapiens

(b) SEQUENCE DESCRIPTION: SEQ ID NO:9599:

ctgtcatgag gtctcttcta tagccatcag gtcttctcac agggatattc accaccttgc 60  
tctggatagg cacatggccg ttgtcagctc tacagtaata ttgcccggca tcaactctctt 120  
tcacagctgg gatctccagc tctgctgaca gggaacgctg ggttttcttt ccataactgg 180  
ttcctgtggc ctctctgtac caggagaatg tgacatttcc tgtaccccca gccactgagc 240  
agagcaggat cagtttttgt ccttcagtca cctgtccccc gggggcccgg atctccaagc 300  
ttacattaga gatggggatt cctagatgga tataagacaa cagggtgagaa ctctaaggga 360  
aactctggga acagggtttg actgattcca ttctctaata caaaatgtgg gaatgtggag 420  
attgtataga taatccatta taagcattcc tatggaggta gggaatctat aacaattatc 480  
cttcaggaat gtggataaag acatttgaat gtcctaacc tgg 523

**SEQ ID NO:9600: LS 368109.1 1908 bp full-length clone**

INFORMATION FOR SEQ ID NO:9600:

(a) SEQUENCE CHARACTERISTICS:

<212> DNA

<213> Homo sapiens

(b) SEQUENCE DESCRIPTION: SEQ ID NO:9600:

gacactcaac ttcacagtgc ctactggggc cagaagcaat catcttacct caggagtcac 60  
tgaggggctg ctcagcacc cttggnccagc caccgtggcc ttattatctt gctacggcct 120  
caaaagaaaa ataggaagac gttcagccag ggatccactc aggagccttc ccagccctct 180  
acccaagag ttcacctacc tcaactcacc taccacaggg cagctacagc ctatatatga 240  
aaatgtgaat gttgtaagt gggatgaggt ttattcactg gcgtactata accagccgga 300  
gcaggaatca gtagcagcag aaaccctggg gacacatatg gaggacaaga tgcagtcact 360  
gaacaggcag attcgtgac ccttgtggcg cctcttctg tcttcgaagg agacagcatc 420  
gttctgaaat gccagggaga acagaactgg aaaattcaga agatggctta ccataaggat 480  
aacaagagat tatctgtttt caagaaaatt ctcagatttc cttatccaaa gtgcagtttt 540  
aagtgcagat ggtaactatt tctgtagtac caaaggacaa ctctttctct gggataaaac 600  
ttcaaatata gtaaagatta aaagtccaag gaatccccat ctctaatagt agcttgagg 660  
tccgggcccc cgggggacag gtgactgaag gacaaaaact gatcctgctc tgctcagtgg 720  
ctgggggtac aggaaatgtc acattctcct ggtacagaga ggccacagga accagtatgg 780  
gaaagaaaac ccagcgttcc ctgtcagcag agctggtaga tcccagctgt gaaagagagt 840  
gatgccggca aatattactg tagagctgac aacggccatg tgcctatcca gagcaagggtg 900  
gtgaatatcc ctgtgagaat tccagtgtct cgccctgtcc tcaccctca ggtctcctgg 960  
ggcccaggct gcagtggggg acctgctgga gcttactgt gaggccctg agaggctctc 1020  
ccccaatctt gtaccaattt tatcatgagg atgtcaccct tgggaacagc tcggccctc 1080  
tggaggaggg gctccttca acctctctt gactgcagaa cattctggaa actactcctg 1140

tgaggccaac	aacggcctgg	gggcccagtg	caggtggagg	gcagtgccag	gtcctccatc	1200
tcaggacctg	atggctatag	aaagagacct	catgacagct	ggagtctctc	ggggacctgt	1260
ttggtgtcct	tgcgttcact	gggtgttgct	ttgctgttgt	atgccttggt	ccacaagata	1320
tcaggagaaa	gttctgccac	taatgaaccc	agaggggctt	ccaggccaaa	tcctcaagag	1380
ttcacctatt	caagcccaac	cccagacatg	gaggagctgc	agccacgtgt	atgtcaatgt	1440
gggctctgta	gatgtggatg	tggtttattc	tcaggtctgg	agcatgcagc	agccagaaaag	1500
ctcagcaaac	atcaggacac	ttctggagaa	caaggactcc	caagtcatct	actcttctgt	1560
gaagaaatca	taacacttgg	aggaatcaga	aggggaagatc	aacagcaagg	atggggcatc	1620
attaagactt	gctataaaac	cttatgaaaa	tgcttgaggc	ttatcacctg	ccacagccag	1680
aacgtgcctc	aggaggcacc	tcctgtcatt	tttgtcctga	tgatgtttct	tctccaatat	1740
cttctttttac	ctatcaatat	tcattgaact	gctgctacat	ccagacactg	tgcaaataaa	1800
ttattttctgc	tacctttctc	taagcaatca	gtgtgtaaag	atttgaggga	agaatgaata	1860
agagatacaa	ggtctcacct	tcatctactg	tgaagtgatg	agaacagg		1908

**SEQ ID NO:9611: Ly1448 protein**

(a) SEQUENCE CHARACTERISTICS:

(b) SEQUENCE DESCRIPTION: SEQ ID NO:9611:

Lys Ile Ser Gly Glu Ser Ser Ala Thr Asn Glu Pro Arg Gly Ala Ser  
 180 185 190  
 Arg Pro Asn Pro Gln Glu Phe Thr Tyr Ser Ser Pro Thr Pro Asp Met  
 195 200 205  
 Glu Glu Leu Gln Pro Val Tyr Val Asn Val Gly Ser Val Asp Val Asp  
 210 215 220  
 Val Val Tyr Ser Gln Val Trp Ser Met Gln Gln Pro Glu Ser Ser Ala  
 225 230 235 240  
 Asn Ile Arg Thr Leu Leu Glu Asn Lys Asp Ser Gln Val Ile Tyr Ser  
 245 250 255  
 Ser Val Lys Lys Ser  
 260

**SEQ ID NO:10,467: Ra12-Ly1464 fusion cDNA sequence (see, Example 7)**

atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccaggggtggg 60  
 cagggattcg ccattccgat cgggcaaggc atggcgatcg cgggccagat caagcttccc 120  
 accgttcata tcgggcctac cgccttcctc ggcttggttg ttgtcgacaa caacggcaac 180  
 ggcgacagag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240  
 ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300  
 gcgcttaacg ggcacatcat cgggtgacgt atctcggtga cctggcaaac caagtcgggc 360  
 ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt ctccatggac 420  
 atgaagctgg gctgtgtcct catggccttg gccctctacc tttcccttgg tgtgtctctg 480  
 gtggcccaga tgctactggc tgccagtttt gagacgtgc agtgtgaggg acctgtctgc 540  
 actgaggaga gcagctgcca cacggaggat gacttgactg atgcaaggga agctggcttc 600  
 caggtcaagg cctacacttt cagtgaaccc ttccacctga ttgtgtccta tgactggctg 660  
 atcctccaag gtccagccaa gccagttttt gaaggggacc tgctggttct gcgctgccag 720  
 gcctggcaag actggccact gactcaggtg accttctacc gagatggctc agctctgggt 780  
 cccccgggc ctaacaggga attctccatc accgtggtac aaaaggcaga cagcgggcac 840  
 taccactgca gtggcatctt ccagagccct ggtcctggga tcccagaaac agcatctgtt 900  
 gtggctatca cagtccaaga actgtttcca gcgccaattc tcagagctgt accctcagct 960  
 gaaccccaag caggaagccc catgaccctg agttgtcaga caaagttgcc cctgcagagg 1020  
 tcagctgccc gcctcctctt ctcttctac aaggatggaa ggatagtgca aagcaggggg 1080  
 ctctcctcag aattccagat cccacagct tcagaagatc actccgggtc atactggtgt 1140  
 gaggcagcca ctgaggacaa ccaagtttgg aaacagagcc ccagctaga gatcagagt 1200  
 caggttgctt ccagctctgc tgcacctccc acattgaatc cagctcctca gaaatcagct 1260  
 gctccaggaa ctgctcctga ggaggccctt gggcctctgc ctccgcgcgc aacctcatc 1320  
 tctgaggatc caggcttttc ttctcctctg gggatgccag atcctcatct gtatcaccag 1380  
 atgggccttc ttctcaaaca catgcaggat gtgagagtc tctcgggtca cctgctcatg 1440  
 gagttgaggg aattatctgg ccaccggaag cctgggacca caaaggctac tgctgaatag 1500

**SEQ ID NO:10,468: Ra12-Ly1464 fusion amino acid sequence (see, Example 7)**

Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu  
 5 10 15  
 Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala  
 20 25 30  
 Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala

35	40	45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val		
50	55	60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr		
65	70	75
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr		
85	90	95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser		
100	105	110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr		
115	120	125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Ser Met Asp Met Lys Leu Gly		
130	135	140
Cys Val Leu Met Ala Trp Ala Leu Tyr Leu Ser Leu Gly Val Leu Trp		
145	150	155
Val Ala Gln Met Leu Leu Ala Ala Ser Phe Glu Thr Leu Gln Cys Glu		
165	170	175
Gly Pro Val Cys Thr Glu Glu Ser Ser Cys His Thr Glu Asp Asp Leu		
180	185	190
Thr Asp Ala Arg Glu Ala Gly Phe Gln Val Lys Ala Tyr Thr Phe Ser		
195	200	205
Glu Pro Phe His Leu Ile Val Ser Tyr Asp Trp Leu Ile Leu Gln Gly		
210	215	220
Pro Ala Lys Pro Val Phe Glu Gly Asp Leu Leu Val Leu Arg Cys Gln		
225	230	235
Ala Trp Gln Asp Trp Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly		
245	250	255
Ser Ala Leu Gly Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val		
260	265	270
Val Gln Lys Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln		
275	280	285
Ser Pro Gly Pro Gly Ile Pro Glu Thr Ala Ser Val Val Ala Ile Thr		
290	295	300
Val Gln Glu Leu Phe Pro Ala Pro Ile Leu Arg Ala Val Pro Ser Ala		
305	310	315
Glu Pro Gln Ala Gly Ser Pro Met Thr Leu Ser Cys Gln Thr Lys Leu		
325	330	335
Pro Leu Gln Arg Ser Ala Ala Arg Leu Leu Phe Ser Phe Tyr Lys Asp		
340	345	350
Gly Arg Ile Val Gln Ser Arg Gly Leu Ser Ser Glu Phe Gln Ile Pro		
355	360	365

Thr Ala Ser Glu Asp His Ser Gly Ser Tyr Trp Cys Glu Ala Ala Thr  
370 375 380

Glu Asp Asn Gln Val Trp Lys Gln Ser Pro Gln Leu Glu Ile Arg Val  
385 390 395 400

Gln Gly Ala Ser Ser Ser Ala Ala Pro Pro Thr Leu Asn Pro Ala Pro  
405 410 415

Gln Lys Ser Ala Ala Pro Gly Thr Ala Pro Glu Glu Ala Pro Gly Pro  
420 425 430

Leu Pro Pro Pro Pro Thr Pro Ser Ser Glu Asp Pro Gly Phe Ser Ser  
435 440 445

Pro Leu Gly Met Pro Asp Pro His Leu Tyr His Gln Met Gly Leu Leu  
450 455 460

Leu Lys His Met Gln Asp Val Arg Val Leu Leu Gly His Leu Leu Met  
465 470 475 480

Glu Leu Arg Glu Leu Ser Gly His Arg Lys Pro Gly Thr Thr Lys Ala  
485 490 495

Thr Ala Glu

**SEQ ID NO:10,469: LS 238330.1 (see, Example 9)**

<210> 4  
<211> 1442  
<212> DNA  
<213> Homo sapiens

<400> 4  
gcgtgaggca ccgcggctgg cctgagtttc ttcttaatac tgtatcacaa ttgtgggctg 60  
tcttatgtgt tgatatcgat tgagctatth gaaataggaa tgttaatggg tgtattaaat 120  
ttttgtaagg atataacaat atctaccttc caaggatggt gtgaggtttt ccatgatttt 180  
gtatatgagc taatgtttacc tttgaggggt ggtgtgcatt atgttggatg attgttaaatt 240  
ttcagtgga aatgtaccgt gtcctaaatt taaagacatg aaaaatatcc caagatcata 300  
ctagatcata atagcaattc ctttacaaat gaattatgga ggtaactgat ctctaactgat 360  
ttccttcatg ttgttttaat gcacaagggc agaggatctg ctgacccttg gaaccagcgt 420  
gagctaacca cgtgctatag acacttcatg gtgtcgcacc caggggaagtc aaagcgcttt 480  
gctccctcac tgtctgtgag tctcagcca ttagtaccct acccccgct gctccaaaac 540  
ttgagttatt tcaaagtgtt ctactgttc atctctccac tgaccctact ccagaaagcc 600  
tggagagagt cccaagatgc caccacctt cccaatccc tcgccacaga tctgtgtcta 660  
tctcacactc tgtaagtgcc gctttgcttc ttctctctt gaaaagactg agaacacaca 720  
ttttaacatg ttaggaaaat ggggcagcct aaaaaatgac tgatcccacc gccagtgact 780  
catgtatact ccaggctagc agacaaggcc ctttttggtg ggctgtctt tgtgggttca 840  
cagaaaccaa attactgtgg gttgcaaaga attagcagg catttacaaa gcagacatcc 900  
cttcacccag actgtggtt tgcattgctc gggtctcagt ctatgagctt tgggtgcagg 960  
tcattttggc tactggaaaa accatagctt attttaaatt tctggttgcc aaagccacca 1020  
cacgtgtggt ctgtggatga ccattgtctg cagaatgacg aggaaggaa acagaatgtgt 1080  
ttggggctca ggggtgacct cccactggga ggggaaggcg gagggagccc ttgcctggg 1140  
ttttgacaca gctgtgtct acagcctctc ctctcatctg catttctcag aaatgcctc 1200  
cctgcccagt ggtgactttt cctcgtcact cctatggagt tctacctgga gccagccat 1260  
gtgtggaact gtgaagttaa ctctctgta aagatggttt aaagaaagtc agcttctgaa 1320  
atgtaacaat gctaaccctt gctggaacct tgtaagaaat agcctgctg atagttttct 1380  
aggtttatca tgtttgattt ttactgaa aaataaaaa atcctggtat gtttgaaaa 1440  
aa 1442

**SEQ ID NO:10,470: Ly1456P FL contig (see, Example 9)**

```
<210> 5
<211> 1637
<212> DNA
<213> Homo sapiens
```

<400> 5						
acctcctggg	ctcaagcaac	gagccatcct	cccgctcttag	cctcccaact	agctgagact	60
acaggcgtgg	gtcaccacac	ccagctaatt	tttgtacttt	ttgtagagac	agggctctcac	120
catggtgccc	aggctgggtc	tgaactcctg	ggctcaagta	atctgccac	ctcagcctcc	180
caaagtgttg	gggttacagg	cgtgaggcac	cgcggctggc	ctgagtttct	tcttaatact	240
gtatcacaa	tgtgggctgt	cttatgtgtt	gatatcgatt	gagctatttg	aaataggaat	300
gttaatgggt	gtattaaatt	tttgtaaagg	tataacaata	tctaccttcc	aaggatgttg	360
tgagggtttt	catgattttg	tatatgagct	aatgttacct	ttgaggggtg	gtgtgcatta	420
tgttggatga	ttgtaaattt	tcagtggaaa	atgtaccgtg	tcctaaattt	aaagacatga	480
aaaatatccc	aagatcatac	tagatcataa	tagcaattcc	tttacaaatg	aattatggag	540
gtaactgata	tctaacagtt	tccttcatgt	tgttttaatg	cacaagggca	gaggatctgc	600
tgacctttgg	aaccagcgtg	agctaaccac	gtgctataga	cacttcatgg	tgctcgaccc	660
agggaagtca	aagcgctttg	ctccctcact	gtctgtgagt	cctcagccat	tagtacccca	720
cccccgctg	ctccaaaact	tgagttattt	caaatgtttc	tctactgtta	tctctccact	780
gacccccact	cagaaagcct	ggagagagtc	ccaagatgcc	accaccttc	cccaatccct	840
cgccacagat	ctgtgtctat	ctcacactct	gtaagtgccg	ctttgcttct	tctctctctg	900
aaaagactga	gaacacacat	tttaacatgt	taggaaaatg	gggcagccta	aaaaatgact	960
gatcccaccg	ccagtgactc	atgtatactc	caggctagca	gacaaggccc	tttttggtgg	1020
gcctgcttct	gtgggttcac	agaaaacaaa	ttactgtggg	ttgcaaagaa	ttagcagggtc	1080
atttacaaag	cagacatacc	ttcaccacga	ctgtggtttt	gcattgctcag	gttctcagtc	1140
catgagcttt	ggtgcaggat	cattttggct	actggaaaaa	ccatagctta	tttttaattt	1200
ctggttgcca	aagccaccac	acgtgtggtc	tgtggatgac	cattgtctgc	agaatgacga	1260
ggaaggaaca	gaatgtgggt	tggggctcag	ggtggccttc	ccactgggag	ggaaggcggg	1320
agggagccct	tgccctgggt	tttgacacag	cctgtgctca	cagcctctcc	tctcatctgc	1380
atttctcaga	aatgccctcc	ctgccagtg	gtgactttcc	ctcgtcactc	ctatggagtt	1440
ctacctggag	cccagccatg	tgtggaactg	tgaagtttac	tcctctgtaa	agatggttta	1500
aagaaggtca	gctttctgaa	tgtaacaatg	ctaacccttg	ctggaaccct	gtaagaaata	1560
gcctagctga	tagttttcta	ggtttatcat	gtttgatttt	tacactgaaa	aataaaaaaa	1620
tccctgatatg	tttqaaa					1637

**SEQ ID NO:10,471: Lv1456P FL contig ORF1 (see, Example 9)**

```
<210> 6
<211> 98
<212> PRT
<213> Homo sapiens
```

```

<400> 6
Met His Lys Gly Arg Gly Ser Ala Asp Pro Trp Asn Gln Arg Glu Leu
           5              10              15

Thr Thr Cys Tyr Arg His Phe Met Val Ser His Pro Gly Lys Ser Lys
           20              25              30

Arg Phe Ala Pro Ser Leu Ser Val Ser Pro Gln Pro Leu Val Pro His
           35              40              45

Pro Pro Leu Leu Gln Asn Leu Ser Tyr Phe Lys Cys Phe Ser Leu Phe
           50              55              60

Ile Ser Pro Leu Thr Pro Leu Gln Lys Ala Trp Arg Glu Ser Gln Asp

```





<213> Homo sapiens

<400> 9

Met Trp Phe Gly Ala Gln Gly Gly Leu Pro Thr Gly Arg Glu Gly Gly  
5 10 15  
Arg Glu Pro Leu Pro Trp Val Leu Thr Gln Pro Val Leu Thr Ala Ser  
20 25 30  
Pro Leu Ile Cys Ile Ser Gln Lys Cys Pro Pro Cys Pro Val Val Thr  
35 40 45  
Phe Pro Arg His Ser Tyr Gly Val Leu Pro Gly Ala Gln Pro Cys Val  
50 55 60  
Glu Leu  
65

**SEQ ID NO:10,475:**

**GenBank clone on chromosome 15q21 clone b2265b18 (acc. no. AC008131)**

see Figure 24 for sequence

**SEQ ID NO:10,476**

**human secreted protein-encoding gene 9 cDNA clone HTOHB55 SEQ ID NO:1 (acc. no. AAH19210)**

see Figure 25 for sequence

**SEQ ID NO:10,477**

**human secreted protein-encoding gene 9 cDNA clone HTOHB55 SEQ ID NO:19 (acc. no. AAH19178) on chromosome 15q21**

see Figure 26 for sequence

**SEQ ID NO:10,478**

**lung cancer associated polynucleotide sequence SQID 265 (Genseq accession number AAF18246)**

see Figure 29 for sequence

**SEQ ID NO:10, 479**

**homo sapiens Genbank clone on chromosome 17 clone RP11-956N15 (accession number AC021581)**

see Figure 30 for sequence

**SEQ ID NO:10,480: Template LS 1076101.8 HERV nucleotide sequence**

**(see, Example 11)**

gccgctgccg ctccaggaga caggttccca tgcaggaatg aaagacatgg aaggggaagag 60  
ggggggccagc tccctgagtc ctgtgtccac cagctgctgc taaatacctc tgagaaactc 120  
tgcttctatc taagggggacc tacttctctc gggaatctca atacttgga caagaacctc 180  
ctagacggac cctttggcat aatgaattgg accaactgta ggttccagga ctagagagcc 240  
agcaatgcct ccatgaacaa tctcacccaa ttactctgct caggaaacga ggtaactgat 300  
ggacagccga ggcagccccct taggcggctt aggcctcccc tgtggagcat ccctgaggcg 360  
gactccggcc agcccagtg atgcatcca aagagcactc ccgggtagga aattgccccg 420  
gtggaatgcc tcaccagagc agcgtgtagc agttccctgt ggaggattaa cacagtggct 480  
gaacaccggg aaggaactgg cacttggagt ccggacatct gaaacttgta gactgggagc 540  
tgtacatgga tgggagcagc ttcaccaacc cctgcaaagt gactctgaag aagacgacaa 600  
gccctgctcc agtcacaccc ggaagctgac tgggtccacgc acagctgaag catgaggaaa 660  
ctcatcgagg gactaatttt ccttaaaatt tagacttgca cagtaaggac ttcaactgac 720  
cttctcaga ctgagaactg tttccagtat atacatcaag tcaactgaggt aggacaaaag 780  
attgctacat tcctattatt ttaaggttac atttttgggg acccctcttt cttctgttct 840  
agctattacc tttcttgtgt cacctagaaa aggaccagtc cttaattgta ttttaaaaac 900  
tgtgatcatg ggaagcttta aattggttca ataacacgca tcaagttggt tatttctctg 960  
gctacatacc ttgatagat 980

**SEQ ID NO:10,481: Template LS 1076101.8 HERV amino acid sequence**

**(see, Example 11)**

Met Asp Ser Arg Gly Ser Pro Leu Gly Gly Leu Gly Leu Pro Cys Gly  
5 10 15  
Ala Ser Leu Arg Arg Thr Pro Ala Ser Pro Ser Asp Ala Ile Gln Arg  
20 25 30  
Ala Leu Pro Gly Arg Lys Leu Pro Arg Trp Asn Ala Ser Pro Glu Gln  
35 40 45  
Arg Val Ala Val Pro Cys Gly Gly Leu Thr Gln Trp Leu Asn Thr Gly  
50 55 60  
Lys Glu Leu Ala Leu Gly Val Arg Thr Ser Glu Thr Cys Arg Leu Gly  
65 70 75 80  
Ala Val His Gly Trp Glu Gln Leu His Gln Pro Leu Gln Ser Asp Ser  
85 90 95  
Glu Glu Asp Asp Lys Pro Cys Ser Ser His Thr Arg Lys Leu Thr Gly  
100 105 110  
Pro Arg Thr Ala Glu Ala  
115

**SEQ ID NO:10,482: LS-1452 with His tag nucleotide sequence (see, Example 13)**

atgcagcatc accaccatca ccacgtgtca caatctacag tcaggcagga ttctctgtg 60  
gagccctggg aagggatcag cgatcactct ggcattattg atggttcgcc cagactcctg 120  
aacactgacc atcctccttg ccaattagac atcaggtctca tgaggcacia agctgtctgg 180  
attaaccccc aggatgtgca gcaacagccg caggacttgc aatctcaggt gccagcagca 240

```

gggaacagtg ggacccattt tgtgacagat gctgcctctc cctcaggccc ttcaccttcg 300
tgccctcgagg actccctggc agagacaacg ttgtctgagg ataccacaga ctccgttggc 360
agcgcttctc cccatggctc gagtgaaaag agtagcagct tctctctgtc ctcaacagag 420
gtacacatgg tccgcccagg atactctcat cgggtgtctc tgcccacaag ccctgggatt 480
ttggccacct ccccatatcc tgagactgac agtgcttttt ttgagccttc ccatctgaca 540
tctgctgctg atgaagggtc tgttcaagtc agtagaagaa ccatttcttc gaattccttc 600
tcaccagagg tatttgtgct gcctgttgat gtagaaaagg aaaatgccc cttttatgtt 660
gcagatatga ttatatcagc aatggagaaa atgaagtgtg acattctgag tcaacagcag 720
acagagagct ggagtaaaga agtcagtggg ttacttggga gtgatcagcc tgactctgaa 780
atgacttttg ataccaacat aaagcaagag tctgggtctt ctacttcttc atacagtggc 840
tatgaagggt gtgctgtgtt acaggtcagc ccagtgtactg aaacacgtac ttaccatgat 900
gtgaaagaga ttgcaaagt cgatgttgat gaatttgta ttttagagct tggagatttt 960
aatgatatac cagaaacctg tagctgttcc tgcagctcct ctaagagtgt cacttatgag 1020
ccagacttca attctgcaga actattagcc aaagagctgt accgcgtgtt ccagaagtgc 1080
tggatactgt cagtagttaa ttctcagctg gcaggttccc tgagtgcagc tggctcgata 1140
gtcgtaaatg aagagtgtgt ccgaaaagac tttgaatcca gtatgaatgt agtacaggaa 1200
attaaattta agtctaggat cagagggact gaagactggg ctccctctag atttcaaadc 1260
atattttaata ttcattccacc actcaagagg gaccttgtgg tggcagccca gaattttttc 1320
tgtgccggct gtggaactcc agtagagcct aagtttgtga agcggctccg gtactgcaaa 1380
tacctaggga agtatttctg tgactgtctg cactcatatg cagagtctgt catccctgcc 1440
cgaatcctga tgatgtggga cttcaagaag tactacgtca gcaatttctc caaacagctg 1500
ctcgacagca tatggcacca gccatttttc aatttgtgta gcatcggcca aagcctgtat 1560
gcgaaagcca aggagctgga cagagtgaag gaaattcagg agcagctctt ccatatcaag 1620
aagctgttga agacctgtag gtttgctaac agtgcattaa aggagtccga gcagggtgccg 1680
ggacacttga ctgatgagct ccacctgttc tcccttgagg acctggtcag gatcaagaaa 1740
gggctgctgg cacccttact caaggacatt ctgaaagctt cccttgacac tgtggctggc 1800
tgtgagctgt gtcaaggaaa gggctttatt tgtgaatttt gccagaatac gactgtcatc 1860
ttcccatctc agacagcaac atgtagaaga tgttcagcgt gcagggtctg ctttcacaaa 1920
cagtgtcttc agtcctccga gtgcccccg tgtgagagga tcacagcgag gagaaaactt 1980
ctggaaaagtg tggcctctgc agcaaca 2007

```

**SEQ ID NO:10,483: LS-1452 with His tag amino acid sequence (see, Example 13)**

```

Met Gln His His His His His Val Ser Gln Ser Thr Val Arg Gln
                    5              10              15
Asp Ser Pro Val Glu Pro Trp Glu Gly Ile Ser Asp His Ser Gly Ile
                20              25              30
Ile Asp Gly Ser Pro Arg Leu Leu Asn Thr Asp His Pro Pro Cys Gln
                35              40              45
Leu Asp Ile Arg Leu Met Arg His Lys Ala Val Trp Ile Asn Pro Gln
                50              55              60
Asp Val Gln Gln Gln Pro Gln Asp Leu Gln Ser Gln Val Pro Ala Ala
                65              70              75              80
Gly Asn Ser Gly Thr His Phe Val Thr Asp Ala Ala Ser Pro Ser Gly

```

	85	90	95
Pro Ser Pro Ser Cys Leu Gly Asp Ser Leu Ala Glu Thr Thr Leu Ser			
	100	105	110
Glu Asp Thr Thr Asp Ser Val Gly Ser Ala Ser Pro His Gly Ser Ser			
	115	120	125
Glu Lys Ser Ser Ser Phe Ser Leu Ser Ser Thr Glu Val His Met Val			
	130	135	140
Arg Pro Gly Tyr Ser His Arg Val Ser Leu Pro Thr Ser Pro Gly Ile			
	145	150	155
Leu Ala Thr Ser Pro Tyr Pro Glu Thr Asp Ser Ala Phe Phe Glu Pro			
	165	170	175
Ser His Leu Thr Ser Ala Ala Asp Glu Gly Ala Val Gln Val Ser Arg			
	180	185	190
Arg Thr Ile Ser Ser Asn Ser Phe Ser Pro Glu Val Phe Val Leu Pro			
	195	200	205
Val Asp Val Glu Lys Glu Asn Ala His Phe Tyr Val Ala Asp Met Ile			
	210	215	220
Ile Ser Ala Met Glu Lys Met Lys Cys Asn Ile Leu Ser Gln Gln Gln			
	225	230	235
Thr Glu Ser Trp Ser Lys Glu Val Ser Gly Leu Leu Gly Ser Asp Gln			
	245	250	255
Pro Asp Ser Glu Met Thr Phe Asp Thr Asn Ile Lys Gln Glu Ser Gly			
	260	265	270
Ser Ser Thr Ser Ser Tyr Ser Gly Tyr Glu Gly Cys Ala Val Leu Gln			
	275	280	285
Val Ser Pro Val Thr Glu Thr Arg Thr Tyr His Asp Val Lys Glu Ile			
	290	295	300
Cys Lys Cys Asp Val Asp Glu Phe Val Ile Leu Glu Leu Gly Asp Phe			
	305	310	315
Asn Asp Ile Thr Glu Thr Cys Ser Cys Ser Cys Ser Ser Ser Lys Ser			
	325	330	335
Val Thr Tyr Glu Pro Asp Phe Asn Ser Ala Glu Leu Leu Ala Lys Glu			
	340	345	350
Leu Tyr Arg Val Phe Gln Lys Cys Trp Ile Leu Ser Val Val Asn Ser			
	355	360	365
Gln Leu Ala Gly Ser Leu Ser Ala Ala Gly Ser Ile Val Val Asn Glu			
	370	375	380
Glu Cys Val Arg Lys Asp Phe Glu Ser Ser Met Asn Val Val Gln Glu			
	385	390	395
Ile Lys Phe Lys Ser Arg Ile Arg Gly Thr Glu Asp Trp Ala Pro Pro			
	405	410	415
Arg Phe Gln Ile Ile Phe Asn Ile His Pro Pro Leu Lys Arg Asp Leu			
	420	425	430
Val Val Ala Ala Gln Asn Phe Phe Cys Ala Gly Cys Gly Thr Pro Val			
	435	440	445

Glu Pro Lys Phe Val Lys Arg Leu Arg Tyr Cys Glu Tyr Leu Gly Lys  
 450 455 460  
 Tyr Phe Cys Asp Cys Cys His Ser Tyr Ala Glu Ser Cys Ile Pro Ala  
 465 470 475 480  
 Arg Ile Leu Met Met Trp Asp Phe Lys Lys Tyr Tyr Val Ser Asn Phe  
 485 490 495  
 Ser Lys Gln Leu Leu Asp Ser Ile Trp His Gln Pro Ile Phe Asn Leu  
 500 505 510  
 Leu Ser Ile Gly Gln Ser Leu Tyr Ala Lys Ala Lys Glu Leu Asp Arg  
 515 520 525  
 Val Lys Glu Ile Gln Glu Gln Leu Phe His Ile Lys Lys Leu Leu Lys  
 530 535 540  
 Thr Cys Arg Phe Ala Asn Ser Ala Leu Lys Glu Phe Glu Gln Val Pro  
 545 550 555 560  
 Gly His Leu Thr Asp Glu Leu His Leu Phe Ser Leu Glu Asp Leu Val  
 565 570 575  
 Arg Ile Lys Lys Gly Leu Leu Ala Pro Leu Leu Lys Asp Ile Leu Lys  
 580 585 590  
 Ala Ser Leu Ala His Val Ala Gly Cys Glu Leu Cys Gln Gly Lys Gly  
 595 600 605  
 Phe Ile Cys Glu Phe Cys Gln Asn Thr Thr Val Ile Phe Pro Phe Gln  
 610 615 620  
 Thr Ala Thr Cys Arg Arg Cys Ser Ala Cys Arg Ala Cys Phe His Lys  
 625 630 635 640  
 Gln Cys Phe Gln Ser Ser Glu Cys Pro Arg Cys Ala Arg Ile Thr Ala  
 645 650 655  
 Arg Arg Lys Leu Leu Glu Ser Val Ala Ser Ala Ala Thr  
 660 665

**SEQ ID NO:10,484: TCL-1 with His tag nucleotide sequence (see, Example 13)**

atgcagcatc accaccatca ccacgccgag tgcccgacac tcggggaggc agtcaccgac 60  
 caccgcgacc gcctgtgggc ctgggagaag ttcgtgtatt tggacgagaa gcagcacgcc 120  
 tggtgcct taaccatcga gataaaggat aggttacagt tacgggtgct cttgcgtcgg 180  
 gaagacgtcg tcctggggag gcctatgacc cccaccaga taggccaag cctgctgcct 240  
 atcatgtggc agctctaccc tgatggacga taccgatcct cagactccag tttctggcgc 300  
 ttagtgtacc acatcaagat tgacggcgtg gaggacatgc ttctcgagct gctgccagat 360  
 gactgatga  
 369

**SEQ ID NO:10,485: TCL-1 with His tag amino acid sequence (see, Example 13)**

Met Gln His His His His His His Ala Glu Cys Pro Thr Leu Gly Glu  
 5 10 15  
 Ala Val Thr Asp His Pro Asp Arg Leu Trp Ala Trp Glu Lys Phe Val  
 20 25 30

Tyr Leu Asp Glu Lys Gln His Ala Trp Leu Pro Leu Thr Ile Glu Ile  
 35 40 45  
 Lys Asp Arg Leu Gln Leu Arg Val Leu Leu Arg Arg Glu Asp Val Val  
 50 55 60  
 Leu Gly Arg Pro Met Thr Pro Thr Gln Ile Gly Pro Ser Leu Leu Pro  
 65 70 75 80  
 Ile Met Trp Gln Leu Tyr Pro Asp Gly Arg Tyr Arg Ser Ser Asp Ser  
 85 90 95  
 Ser Phe Trp Arg Leu Val Tyr His Ile Lys Ile Asp Gly Val Glu Asp  
 100 105 110  
 Met Leu Leu Glu Leu Leu Pro Asp Asp  
 115 120

### Sequences Listed in Figure 5- Highly expressed in lymphoma cells

#### SEQ ID NO: 10,486

gtgaaacacc ctcggccggg aagtcagttc gttctctcct ctctctctctt cttgtttgaa 60  
 catggtgcgg actaaagcag acagtgttcc aggcacttac agaaaagtgg tggctgctcg 120  
 agccccaga aaggtgcttg gttcttccac ctctgccact aattcgacat cagtttcatc 180  
 gaggaaagct gaaaataaat atgcaggagg gaaccccggt tgcgtgcgcc caactcccaa 240  
 gtggcaaaaa ggaattggag aattcttttag gttgtcccct aaagattctg aaaaagagaa 300  
 tcagattcct gaagaggcag gaagcagtgg cttaggaaaa gcaaagagaa aagcatgtcc 360  
 tttgcaacct gatcacacaa atgatgaaaa agaatagaac tttctcattc atctttgaat 420  
 aacgtctcct tgtttaccct ggtattctag aatgtaaatt tacataaatg tgtttgttcc 480  
 aattagcttt gttgaacagg catttaatta aaaaatttag gttt 524

#### SEQ ID NO: 10,487

ctgcttgtag ttcaaagccc tccgtctagc catctcagcc aggtcaggt tccttctccc 60  
 acccatcagg ccaagcagga cttgtcaaac atacacattc aagttcctag cacacagtag 120  
 gtgctaagtg ggaattgatt ataaacttga attcttccat caacaaatat ccacctctcc 180  
 tgtccagctt gcctcagatc ttcaggttct ctcttctctg aggcagctaa gcttctacat 240  
 ccttcatgaa gtttccttta cttctcgaca gaagacagtt ccctttagg 289

#### SEQ ID NO: 10,488

ccattagctc ctgtagctag ttctgtctt ttccaaaacc tgtttttttt ttggcttttt 60  
 ggtagatgct gtggctctct tatggcctcc aataaacata agtgaggcag agttgggtttc 120  
 tattgtttgc aaccaacgaa cttaatggat tctgtattag aaagaactgg tatatttctt 180  
 taagcaaaga ctaggactct atggggctca acaaactctg taatcgctt tccactcccc 240  
 tggacaaaat aaatatattg tctactgctg aaacgcaaat tatccccaaa ccaagtagct 300  
 tt 302

#### SEQ ID NO: 10,489

tataaactgt ggcgggatag ttttcgggtc cttgtccagt gaaacaccct cggccgggaa 60  
 gtcagttcgt tctctcctct cctctcttct tgtttgaaca tgggtgcggac taaagcagac 120  
 agtggtccag gcacttacag aaaagtgggt gctgctcgag cccccagaaa ggtgcttggt 180  
 tcttccacct ctgccactaa ttcgacatca gtttcatcga ggaaagctga aaataaatat 240  
 gcaggaggga accccggttg cgtgcgcccc actcccaagt ggcaaaaagg aattggagaa 300  
 ttcttttaggt tgtcccctaa agattctgaa aaagagaatc agattcctga agaggcagga 360  
 agcagtggtt taggaaaagc aaagagaaaa gcatgtcctt tgcaacctga tcacacaaat 420

gatgaaaaag aatagaactt tctcattcat ctttgaataa cgtctccttg tttaccctgg 480  
tattctagaa tgtaaattta cataaatgtg tttgttccaa ttagctttgt tgaacaggca 540  
tttaattaaa aaatttaggt tt 562

**SEQ ID NO: 10,490**

ctgcttggac ttcaaagccc tccgcctagc catctcagcc aggetcaggt tccttctccc 60  
acccatcagg ccaagcagga cttgtcaaac atacacattc aagttcctag cacacagtag 120  
gtgctaagt ggaattgatt ataaacttga attcttccat caacaaatat ccacctctcc 180  
tgtccagctt gcctcagatc ttcaggttct ctcttctctg aggcagctaa gcttctacat 240  
ccttcagtaa gtttctctta cttctcgaca gaagacaggt cccttttagg 289

**SEQ ID NO: 10,491**

aaaaaaaaa aacaaagcaa agcaaagcaa aacaaaacag ctctttataa tgtacaatgg 60  
cttaagcaaa tcgcttttagt tttttttcta ttttaagattt aggacagact actcgtctaa 120  
aattcactat ttacagagaa ggtcctaggg aacaggataa cttatttagg tttagctctc 180  
ataatacaat atccataatg gctttagaag aatgtaaata aataacattg gtaaacagcg 240  
tatactgata ttttctgaca aactcattta tctaactca tgctgagcaa tcaagaggat 300  
tcctctatat atttt 315

**SEQ ID NO: 10,492**

aaaaaaaaa tcaaaagcag acatgttttg ctgaaataaa accaagaaac acagctaaaa 60  
ctccccata aacctaaaag tccatggaga attcaatttc tcatttccat tcagaaatct 120  
ggctacaaag tgatttggtt gctatttggtg acagtacaga gtgctgaaag aaaccagct 180  
cttgagtctc ttagatccca tcctgtagga agtggtggga aagccagcgg accatgggca 240  
agtcaactcc tggtacttg gcagggagtc agactgtgct ctctccattc cccaggactc 300  
cacagaacca tctggtactg ctagtgtctg gtgaacagt agagcagagt ccacaaaacg 360  
cagagaacca gaatgtgacc gcaaggagcc aggacctgt gctttttcat ggattacaaa 420  
tctagggcca aggagaggga aagcagaaa agccctattg ggaagaggag ctggctgcgc 480  
ccctaaactg agatggaaa agtaaggctc ttgagccac acctgg 526

**SEQ ID NO: 10,493**

ctgggcaana ccaagtcaca gtttccagcg tgctgtcag ccctccgagt gtgtgtgctc 60  
atccttttca tagaagtccc atmkgscatg gagagggttg ggctgcarag ctgwgattgc 120  
cagaggccct tccttgagaa ctgtggggaa ggaggccctg ggggtttctt ctgtaggcag 180  
agctcaggcc ccagtcacct ctgccacct cagcctggca ctgttggtgc agagcctctg 240  
ctgcctctct ctctctaccc atctgcagac cagcagaata ttctccccct ctcacacca 300  
accaggagtt tggtgtggtt tctggacacg gccagagcag tcaactgcgg gctggttttg 360  
ctgggcttcc ctgtcaaagc aatgctaacg tccagctctc gactcaaggc caggttcttc 420  
tcccacttgt ggctcttggt gcttgagggc tgagccagg gctcctctcc tgctggccgt 480  
ccaggaacag acatcttcac atcctcagtc ttccaaaccc ggacctgccc gtcttgactc 540  
ccggtgatga tgatctggct tgtgtcccat gctgggccct ccatcaggca gcaacagggt 600  
atggctcctt ctgggccccca ggctgtggtg atgtctg 637

**SEQ ID NO: 10,494**

aaacaatgct acactcattt ttggcaaagt gctgtattgt tcagtctgtg tacaaaactg 60  
accatctatg aaccaatcag tataaaaaat ttctataaaa acaaaattta gacagtggct 120  
caagaaaaca agctgccatt tatgcataga ttgatgtaca gtaacctaac caaatgtccc 180  
ttttgaattt tcaagttact gaaaaaaaat gtgtcgagaa acacattaag aaggcacatg 240  
tacagtctac aatactcttc agtctcccta actcatgcc tgcccctata aaggaaatat 300  
gttcacaatt ttacttgaga aaaaaaaaac aagccactta aaaaaaaaac acacacacgc 360  
aattattaaa gttcaaaatc tctggaggaa aatacaagca aaaccactca tacactccaa 420  
gcctgaaaca cacatctaac ctccccaggt actggtttgg ttttcagagg tccacctana 480  
aaacaaatac taaaacttca ggcaaaaacag agcaaaactg gacatttaac aattacacaa 540

ttttt

545

**SEQ ID NO: 10,495**

ctgaataggc	acccaaaagt	ccgtgactaa	atttcgtttg	tctttttgat	agcaaattat	60
gttaagagac	agtgatggct	agggctcaac	aattttgtat	tcccatgttt	gtgtgagaca	120
gagtttgttt	tcccttgaac	ttgggttagaa	ttgtgctact	gtgaacgctg	atcctgcata	180
tggaagtccc	gcttcggtga	catttcctgg				210

**SEQ ID NO: 10,496**

cctcctcgac	caaggcaggg	aacttcaatc	tgtataagta	tctgcagttg	ctggaataat	60
ttgaagaccc	catggagcta	aggagattaa	gtggaggatt	ttcattgttt	cagaggggca	120
aggggcaaat	ccattgctaa	ttctttaatg	atgaaaaatg	gtaagaagtt	gttaaaactcc	180
tttggggatt	ttaaaaagtg	atacgtaaac	agaagagaga	gagagagaga	gaaatcacag	240
tagtgaggct	aacaaaaata	atgataaaaa	ggttagaaga	accaggata	cttagtggat	300
gcctagacaa	cataaaaaata	gatttataga	aggaagcaat	ggaatttgaa	tataaaaggg	360
tatcagaaaag	ttaatgtgtt	gcatctgaaa	ttcaaagtat	ttccttttgg	ctacacaaga	420
aagactttta	ataaaaccct	ttgtatatat	ttctgaaagg	naaatatttt	atagggaaat	480
ggaggattgg	aagaaaatct	gttccatcat	gtctgggtat	tagaattttg	cttaataact	540
tgccaaaata	ttacgcttcc	aagggtcatg	gcattatgtg	tgtaccaaat	taaag	595

**SEQ ID NO: 10,497**

ctgtggctgt	ctgtcagaga	agcacatttt	tctgcagata	attagaatgg	cttcccccat	60
ctctcacgga	ctgtcccaag	tctagaaaag	aattgagttc	ctcttctatt	agtcaataaa	120
aagggaagag	aatgtttgtc	ttcctttcct	ttctgtagtg	ttaagaaaat	aaacgaactt	180
aatgattcta	aattatcagt	gagcttaaca	ctgtactata	gaccaaagat	taccttttca	240
aaaagtccct	tgagggtgaaa	tattttgtat	acgtaataca	tagatgcaca	tataaacaca	300
cacatataga	atctcaatat	tttaacactt	ctttgggtag	ttgtactaac	tcactaaccc	360
tgaggaaaaa	gttaagaaat	tgaaagtgtt	ttcttcaaaa	gttgagattt	aacaataaaa	420
ggtgttactt	tgataactaa	aaggaaactt	attatcctct	tcctaaaata	aaccaatgcc	480
tattctgaaa	atggcacttg	caattacaat	ttgccattat	caaagctacc	actgaggtag	540
aggcattatc	taaaacaaat	accacttatc	atattattggc	agttacctcg	agagagaccc	600
atacaccatc	ttctagcaga	gcacagtcaa	tcaaattacc	ttcgggtaaa	gctatagcat	660
gtctagtctg	ttgacagata	ttaaagggtg	tcataaaaga	aacataaacc	ataggctgtg	720
ctccaaaggc	atattgg					737

**SEQ ID NO: 10,498**

ctgtacgtta	caagtttggg	cattttgaag	cttgacattt	tagtttgcca	ttatgttaaa	60
aacatctaaa	taggtgttag	tttctcagga	gtagattgtt	agtgttgact	tttctgttaa	120
agcagacatc	gttcttggcc	tgccctgcat	tgtatactag	atttcattgt	tgtctctcat	180
gcttcttgag	ttgcttcatg	gtttatgctc	gccatggaaa	gctatcagta	acagtttcat	240
gcttatacca	aagaattaaa	tctgatcttt	aatatctgat	atcttctctg	tactcgtact	300
gataagggat	tattggaagt	cagtcacaga	atcttggaat	aaattctagt	ctctccttag	360
ctatttgatg	cttttcatat	aggccaagaa	ctcattgcaa	aacatttttg	caaggatgaa	420
tgctgtatt	tggtctagga	acagtacatt	ttagtctgat	ttagaattac	tggtagctta	480
ttttaagca	aggaaaagca	g				501

**SEQ ID NO: 10,499**

ccacaagctc	tttagatggg	tacttttagt	aaactcttca	ttcatcctgg	cattcttgaa	60
aatattcgtc	aaacatagag	gaagactcat	cttcacgttc	ctttggttct	ttaaattcta	120
ggtcttctcc	atattgaatg	gcaaaatcaa	tatgctgcaa	tacaatgttc	atgctttctt	180
catctgactg	atcgtaaagg	aaaaatcgaa	ccatgctgta	gtcatcaatc	agtccacata	240



tagcttttagt	cagtttcttg	aattttttgc	ttcttaagtc	acttgtagaa	tcttctaata	300
aagaatacat	gtctggatct	aaaaatttct	caatttcctt	ttttgctttt	ttactcagca	360
gatccatttt	tgctcatgat	ttgacttgcg	gaattttctag	agagatcatg	gcactcaggg	420
ctgccaaagt	gccagaaata	aacttgaatg	actccaccat	gaactgagaa	tcaacaagaa	480
aaactccaca	gactcggaac	tcccactgct	cgagctgctg	gaccagct		528

**SEQ ID NO: 10,500**

actaaacagc	caatcatggg	attcaaagga	cacogtaaag	cagtctctta	tgcaaagttt	60
gtgagtggtg	aggaaattgt	ctctgctca	acagacagtc	agctaaaact	gtggaatgta	120
gggaaacat	actgcctacg	ttccttcaag	ggtcatatca	atgaaaaaaa	ctttgtaggc	180
ctggcttcca	atggagatta	tatagcttgt	ggaagtgaag	ataactctct	ctacctgtac	240
tataaaggac	tttctaagac	tttgctaaat	tttaagtttg	atacagtcaa	aagtgttctc	300
gacaaagacc	gaaaagaaga	tgatacaaat	gaatttggtt	gtgctgtgtg	ctggagggca	360
ctaccagatg	gggagtccaa	tgtgctgatt	gctgctaaca	gtcagggtac	aattaagggtg	420
ctagaattgg	tatgaagggt	taactcaagt	caaattgtac	ttgatcctgc	tgaaatacat	480
ctgcag						486

**SEQ ID NO: 10,501**

cctccccctgc	agctctctgt	gtytgtgatg	atggagctgg	gttggggaaa	tctgtctgtg	60
acatttgccc	tgacgcagtt	ccgcacagca	tggtggcttc	caagctatgc	tcttgatggg	120
cacccgtaag	gagcttctac	atgcattaga	gatggagcct	ctcctatctt	tgcaagcctt	180
tgtgggttct	ccctttaaat	ctgccatcca	cggacctcaa	caggagaata	atttggtctt	240
cagtttgctc	tgtttttagac	aaatacttca	catgactgat	gtaaaactgtt	gcatagtttc	300
acaaaggctt	tctcattcat	tcttgaaatt	ctccatcagt	cacaaacaca	aattgttcag	360
tatctgggga	attcaaagcc	ctttcctcaa	aacagacatt	tctccttatt	attcttcctt	420
caggggaagt	attgaaagtc	attgaaagtc	atccccacc	actagaggag	agaaangcaa	480
gccccagaaa	ggcaagagg	acacagggan	cc			512

**SEQ ID NO: 10,502**

ctgctttctga	tttgacccca	aaatggcacc	acccaaaaaa	acacaaccta	tgctcgggttc	60
ggatttttta	gaagttatct	cagtttaagca	gacactaaag	tacaattata	cttggtctct	120
tgtggcataa	atgatcttga	attttaagat	catttggtct	ttacctattt	agaacaaaac	180
agtctatatt	ttcctgtact	tagaagttgg	aaatgaaata	attttttaaag	cccacaggag	240
attaatttgt	actaagtcac	tactatgtat	caggcattgt	gcttggtgct	ttctagtcac	300
tgaaggagta	ttaaataatg	gaaatgcctg	tcacagtgac	ttgcatgtgg	caatcactca	360
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**SEQ ID NO: 10,503**

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gtaagacaac	atcttaaatc	ttaaaagtgt	tgttatcatg	actggtgaga	gaagaaaaca	180
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agatccctct	ttggagcttt	tttgcatagc	aattaaagg	gtgctatttg	tcagtagcca	360
tttttttgca	gtgatttgaa	gaccaaagtt	gttttacag			399

**SEQ ID NO: 10,504**

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cgtggctctt	ttagaaggca	ggggccagct	accctttgtc	ccagcccagt	gccagccaca	120
gcagggtccc	tggtctctgc	cctctgtgag	ttggtttcac	agacagagcc	agaacactcc	180

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218

**SEQ ID NO: 10,505**

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agaaggtgga ggcaccaggc tcaaaagagg aaatttasaa tytctcattg ggagagtaag 180  
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**SEQ ID NO: 10,506**

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taccttatgg tcttcttta gcaggtaaca aaggagcatc aggggcaggc tgccctgggtg 180  
gcatcacact ggctagttag gccgtgaata tcttgtcccc cagcagggcc gacagtttct 240  
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**SEQ ID NO: 10,507**

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**SEQ ID NO: 10,508**

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**SEQ ID NO: 10,509**

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 aaatcatttt 730

**SEQ ID NO: 10,510**

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**SEQ ID NO: 10,511**

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**SEQ ID NO: 10,512**

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 gaagaagaag aaacagagac gaactttcca gaacctcccc aagatcagga atcctcacca 240  
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**SEQ ID NO: 10,513**

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 gtgacgttga gcgctggtgg gaagaacttg tcaatgtggc agatgagggt gttgggctgg 360  
 ccca 364

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**SEQ ID NO: 10,515**

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**SEQ ID NO: 10,516**

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**SEQ ID NO: 10,518**

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**SEQ ID NO: 10,519**

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**SEQ ID NO: 10,520**

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**SEQ ID NO: 10,521**

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**SEQ ID NO: 10,522**

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**SEQ ID NO: 10,523**

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**SEQ ID NO: 10,524**

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**SEQ ID NO: 10,525**

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**SEQ ID NO: 10,526**

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**SEQ ID NO: 10,527**

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**SEQ ID NO: 10,528**

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**SEQ ID NO: 10,529**

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**SEQ ID NO: 10,530**

10057475.012202

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cttaatgagt	gatctaatac	atttagaatg	ctgaagcact	tctgtggtaa	atgttagtct	300
attctacaat	tgaaaatgcc	tcattttacc	ttttctctaa	actgacaaat	gcaagtagcc	360
agtaactgta	ggcttagaat	tttcggtcac	tgaccagaag	gactaatagg	cgtctatgtg	420
ctcagaacca	ccagtcccgc	accaactctc	ctttcagtga	gcaactgtcag	ccaca	475

**SEQ ID NO: 10,531**

acancctgac	catnaacagg	gnataaacgg	gtcgatgagg	ccgactatta	ctgtcaagtg	60
tgggatcgta	ataatgacca	tgctgtcttc	ggcggaggga	ccaaactggc	cgtcctaggt	120
cagcccaagg	ctgccccctc	ggctactctg	ttcccgcctc	cctctgagga	gcttcaagcc	180
aacaaggcca	cactggtgtg	tctcataant	gactnctacc	cgggagccgt	gacagcggcc	240
tggaaggcag	a					251

**SEQ ID NO: 10,532**

caacatgcct	tctgcatctt	ttaatactac	attcacctga	ttataaatct	ccttctcaga	60
ctctgtaggg	tgggcatttt	caaaatcaag	gaaaaaat	ggccctgct	caaggtctgt	120
gcatgtcaaa	actttaagaa	gattcccat	gttaaggtag	cttcagccag	ygctggbgat	180
tctgtccttg	bccttctatc	cttggtattg	cgttccctct	ttcctagtcc	acttgtttcca	240
gtsccttcaac	ttctg					255

**SEQ ID NO: 10,533**

aaacattcaa	tttattttgtg	gcattttgtac	atgaaaatta	tatgacgata	acattgcttt	60
ctatttctaag	ctagtaaat	gttttctaaga	aataatagat	tgataaaaatt	gcaagtctta	120
atacaaaggt	aggttatgaa	aatgtatatt	aatttgagat	atagaaaagt	tttcaaataa	180
taatgttttc	aggttatat	gcaaatagac	actaaataag	acaaggtttc	tgcaaacatg	240
atgtaacaat	aatgactgga	actctgaatg	tgggaaattc	agaaaatgaa	ccagctactt	300
aaaaagcaaa	aatgtgctaa	gtaaattttgt	attttcatgg	ttatttctaag	gagaggagga	360
ataatctggt	gaggttagtg	ccctcaagca	gaccccataa	ctttgctaca	ccgcatttaa	420
cttctctgtg	ctgttttctt	ttaatttttca	aaatggaaat	tagctgtttc	attgggtgaag	480
tgcattgtaa	aatgagagaa	ttttcaaata	atgcaattac	tctatgggtat	tctgtttttaa	540
tagtaataata	cccatatgaa	gcaggtataa	tgagaataaa	ttttgcccac	aacaaattct	600
gaaatctgaa	gttttggttc	tgctgttata	gtatgaattc	gcttt		645

**SEQ ID NO: 10,534**

ccaatcatag	agatatctgc	accggcctgc	aaagctttcca	tgaacgcttt	gggtcccagac	60
ttggcgatag	taccaagggt	attgatcaag	tcagccttgg	tcattccaat	tccagtatcc	120
acaatagtga	gagttcgatc	ttgtttgttc	ggtataaggt	taatatgcag	ctcttttcca	180
gagtctaatt	tactgggac	tgtcaagctt	tcataccgga	ttttgtccaa	tgcatctgat	240
gaatttgaaa	tgagctctct	cagaaagatc	tctttgttsg	agtagaaaagt	attgatgatc	300
aatgacatca	actgggcaat	ttctgcctga	aaggcgaacg	tctcaacctc	ctcctctctc	360
atcggttggt	cttggtgtctg	ggtttctctc	ggcatcttgg	ctaagtgacc	gcacaggacc	420
aacggcacag	cc					432

**SEQ ID NO: 10,535**

ctgacatgct	ctcaggggtg	aagaagttta	gcttaaaata	cctgatggcg	ctgcataaac	60
tggggatttg	ggaactgagt	ttttagctct	gtgacacaca	acataaaaaa	caaaaatcca	120
gtctcattag	ctaaattcgg	attaaaatct	gaaatgtttt	tatggagttg	ccaacaggct	180
ggaatgtacc	tgatacagtt	taatctgctt	ttattttctt	ggctgtcttc	caaaccactt	240

tcttctgtga attcttaagt tggctagtcc tcttctctca gaaaaattac ccctaagaat 300  
cttcctaata gtgaggggtgt acttccgaat agaagagtcc ttcggctgaa atggcatctc 360  
caagg 365

**SEQ ID NO: 10,536**

ccatgggaat ctaattaatt tcataatgat gttggttgaa catgatacca aaaaatgcag 60  
gtattttcaa gaacaataag atagataaca gcattaaagc ataatccttt aagaattcat 120  
gagaaaaaaa ggatgataaa acttaagctt ctttttcaga tgtttaaaaa tttctataaa 180  
attctttgtc ccaagattaa tcatataacc atggtacata aaatatgcta actacattgc 240  
ctggtgtcaa ggtgggaaaa tcctctttta taacataaaa tcctcttcta atccatgttg 300  
acccaagtcc tggctgtctg agggcagatt cctgtcaaga gacctaaggt tgtcatggaa 360  
agcatcactt tcgtctacta gttggtaatc ctgttccatt tccgttagga agccactccc 420  
agatcctgrc cagagcckga gccggagccg aagcctgatc cagagtagtc ctcakaaagt 480  
gggaagatac gattcaagtc ctggattmtc gc 512

**Sequences Listed in Figure 6-Highly expressed in lymphoma cells**

**SEQ ID NO: 10,537**

aaatatgaat ttgtcttaaa ggcaattcct ttttgttct gtattatctg gaaaagcatg 60  
agagaggcga cacctcaaca aactgatcag agaaaataag cagttactac cctgataggc 120  
accttcccaa tctgtttgct tttgaccatt gtctgtccaa cggacacacc tcaaacaaac 180  
aaaactacca aatagatgac agatcagaat aaagggtgaga ggtctggtcc ccattgaagg 240  
ctgctacagt cttcaaagag gtgaaggagt tcataagaga acaacagtag gaaagttgag 300  
agccaagggt aggagagktg cccaaaagac tccccctact actttagggt actgaaaact 360  
caaaggatca gctacagctt tatctaagta tttactaaat gctacatgag ggtgtccctg 420  
tccagctttc tggcacatga gtccctgtgtg gagagttacc tcctcttcca gggactgtgc 480  
tgttgggaac tttgggcaag tcacttacct ctttgtgcct caatttctgt ataatatctc 540  
taagctacct cactgaggtg gtatgaagat tcactaatgt atgtggcgtg tttgtcaatc 600  
ctccagtga aagcactatc tagatcacat tttggatcac attagccaaa tgcagtaaat 660  
gg 662

**SEQ ID NO: 10,538**

ccaagggagt gagtgggact gaaaatcctg cccctgctcc atgctgagcc acatacaaaag 60  
tccccccagt atattgtggg gccctttctg gcagacatgg agagcttctg aaagtccac 120  
atgcatggaa ttattttcaa gaccccggt atgtggtctg tgggtggtg tctccctgtg 180  
attatggact gagatactca tttagtccca ataagaccag agaagtacat tgtgagatac 240  
gtgggaaacg gctgcatcac tcactgtctt gtgcatgtgt ctccccaggg gcattttcag 300  
atctctgcca cggaggggat gctcttcgag aaggagagat caggtacatt ggaggattca 360  
ttgctgtgg 369

**SEQ ID NO: 10,539**

ctggcatcat ctgagtcttg gaatagcttt cttgtttggt atctgcaaaa agctaggtgg 60  
cctttttagt atcaaatttc aatcttggcc tcactggaac catgctctac agagctttcc 120  
caacagttta gcaagtaagc aaaatcagct tttgctcttc atatttcgta ggtgagactg 180  
gggctttt 188

**SEQ ID NO: 10,540**

aaaatcatte attagcaaaa tatccatcaa ggtagaagct gaaatcatgt tgccatctgc 60  
tgtgaagatg gctgcagttt tgataccctt atcttcattt ttaggttcct gaaggaatga 120  
accaactgtt gacaacattg gtttgactac gaattgacaa cgttcttttc tagatggcaa 180



ggtaagtgtt accaagggaa ggccatgtct ataattaact gttatttcat cag 233

**SEQ ID NO: 10,541**

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 tgtaaggta ttgcaagaat gccaaccct ctggtgtctg atcatgtatc tagcaacatt 120  
 gcagtatgaa gaaaagagat gcccggctc cagcccatgg actagttaat acagtgaagc 180  
 aggttcctgt cttttaccct tcctgctcag aacataaaaag attaaggact aaaatcaagg 240  
 aaggctggga gtttttagagc tggcaaaaatg aagtctaaaa gataaatcaa ggcaacaat 300  
 tactgagaac ttggctgttg cttaacctgg caagtctaaa agcctttctt taaccttgta 360  
 ggaattagat gcataagggt tgctgcaaca tgttcattgg aaacaaacta agtagagctc 420  
 ttatttacia atcttgtaac aaatacttct ggaggaaaaa gagaaaagaa ttcactaagt 480  
 tccanaagac aaagctntaa ttgccagacg tatacaaac 519

**SEQ ID NO: 10,542**

aaattcagaa agatgagaag ctacaatgca actttttttt taatctacag ataccgcaa 60  
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 ccacataaaa tttcatcaga aagtgaact tgattacagc ccaaactaga caaggcaatt 180  
 caggtgcccg gaccccggaag tccacgtgag actacaggag aacgtgcatt atggtgcttg 240  
 ccagccagtc tcttgaggaa ctgcctgtaa cggtcacggg tgtggggaga acaactcca 300  
 ttttttttaa gttttttttt ttatggtatt aaatataagt cttagcacct ttggcatttt 360  
 tgtccaaaca gacttcgaca tatgaagtgg ggacataacc ctcttcacat tcatctctcc 420  
 gaatgcgggt ccagccatcg cctttgtctt cctctatgac atacaatgtt tctccttcaa 480  
 ctacggaaat cgttccttca ttctgacctt caaatgtgta gagagctttg cacgtcccta 540  
 tggcaggagg gggctcctca tcatcaaact cgctgcataa atccgtgg 588

**SEQ ID NO: 10,543**

ccaaaaactg gagtgtctgt ggaaacgcgt tctgccaggc tgcacagcca caaccaaatt 60  
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 ctacgacctc ttgtccctt gagctcagtg aattcccacc aggtgccac agctcctgga 180  
 cttcaaattc tatatattga gagagttgga gagtatatca gagatatttt tggaaaggag 240  
 ttggtctatg caatgtcagt ttggaatctt cttgaaagtt taatgttttt attaggagat 300  
 tt 302

**SEQ ID NO: 10,544**

ctgaattaag tcccttgaga tacacagatg tggtttaact tagttataac atcttgtcat 60  
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 atgcttgat gccctcattt acaagcgatt ttaattactc tcatttaatg gaaacaagtc 180  
 ccaggaaaa gaaaaagaag aaaaatgata cagcaaacca tctgaagcaa tccaagtcct 240  
 atgcttacag tgaccaggt ctactttgct cgaagagAAC actggtactg cattcaaacc 300  
 acaacagaat ccgtcactta actgacctt ctgaattaaa ctgaggtatg aatcaatttg 360  
 aggtatgaac agggaggga aaatgcaata ccagattatg aaaataacca aaatggaaaa 420  
 atttgatgta gaagatatgt ggcttggatt gctccacatc tttggttaaa acatattaag 480  
 aaaagccttt aattacatct gtagtctgaa gcattctaac agacaccagt attccagcaa 540  
 tcttcaaaag atctgtagtg gcaggaaatt aacgccataa aag 583

**SEQ ID NO: 10,545**

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 atacagattt gagaaatgat gctaaattta taggagtttt cagtaactta aaaagctaac 180  
 atgagagcat gccaaaattt gctaagtctt acaaatgata agggctgtcc gcaacaggga 240  
 agaacagttt tgaaaattta tgaactatct tatttttagg taggttttga aagctttttg 300

tctaagtga tttttatgcc ttggtcagag taataactga aggagttgct tatcttggct 360  
ttcgagtcctg agttt 375

**SEQ ID NO: 10,546**

aaactgcaan natttttact tgctagagaa tctgttttaa tatagtgggt tggcctctga 60  
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aactcttggt cacataaaat tgagttgaag ttcatgtgtc cttttttctt ttatccaaat 180  
tttgagttaa agcttcatat ggtaactgca tcctgttcgg acactatagt cttaaattttt 240  
gaaactgtgt ggtgttcgct aaaagtagga ataacaacgt aaaagctaata taagggtcaca 300  
aacttcagtg aaacccttaa aagtcctaat cttcttgata ttgtgaaccg tacccttcc 360  
agtttagttt cttctggact ttccttactt aactgacagt tacctttt 408

**SEQ ID NO: 10,547**

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ttaatatggg aacaccagtt tctagctgtc ctggaggaac caaatcagat gaaaaagtgg 180  
acttgagcaa ggacaaaaaa ttagcccaat ttaacaactg gtttacatgg tgtcataatt 240  
gcaggcacgg tggacatgct ggacatatgc ttagttgggt cagggaccat gcagagtggc 300  
ctgtgtctgc atgcacgtgt aaatgtatgc ag 332

**SEQ ID NO: 10,548**

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aaagagaaat gagggactga tacatgctaa agcatggatg agccttgagc gcatttttgc 120  
caagtgaag aaggcagaca caaaaggcaa cgtattgcat gaggtcattt atatgaaata 180  
tccaaaatag gcaaatccat ggagacagaa agcanataaa tggttgtaag aagctganag 240  
aaaggagtgg ggagagatng ctaaaaagga gtttccttct aggggtgatga aaatgttctg 300  
gaactactta ttggggatga ttgcacaaca tgggtgaagg actcaatgtc nctaattgta 360  
aatttcacat acactttacc ataattttt 389

**SEQ ID NO: 10,549**

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gcttttaagt attattatag acttttggaa actcacgaaa caagcaatcc cttaaattctc 180  
gccaggaaga gtatcttgga ttaaatgggt tttgagaacc ttgagagtgt atattctatg 240  
aaatggaaga aacaagaact agacagagtc acaaatgtct ttgatcacag acaatctctg 300  
ccatccataa ggtaaatgta atacatctgg cgacctgctg agtgtgaact tgcagcag 358

**SEQ ID NO: 10,550**

aaaacataaa ttaataattt ccagtggtatt cccttaaaaa gattacagca gggattttcca 60  
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aggtgaagga ggaagaaagt gtttaggaag tcagtggtgt ccagaagagc tgggtgctggg 180  
tggggcagag tggtagagaga tgctcctttc aaatggaagg ctctggaacc cgccaaaagg 240  
gagtgcaagc tggggcaatc ttcttggaac gccaccagag aaaggcgtca gacccac 298

**SEQ ID NO: 10,551**

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tctgttatc ttgatgaagt gccattttta gcagacactt gtagtgctga ccacttagga 180  
aatgtacaaa ctctaagct tctaaagga ggcattggca aaacgttggg gtcaggatgt 240

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tcttacgttg tgttcacctg ttggttcacc actcagcaga tctgattctg caagaattaa 420
tggtagaact agatcatcct ttctaacaga cgagcctgtg tctgtgacg gcctttcaca 480
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**SEQ ID NO: 10,552**

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ccccatcagc ctctcaccac ctcccagaca cacacaagtc ctcaaaagtt tcagctccgt 180
gtgtgagatg tgcaggtttt ttctaggggg tagggggaga ctaaaatcga atataactta 240
aatgaaaagt atacttttta taatttttct tttt 274

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**SEQ ID NO: 10,553**

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ctactgatga caggatacag tcattagtgt ttatcagctt ctgtattgct gttggaagtt 180
catgctctat tgcagctttt tgactataat gtttggaagt atctttcata acgtcatgaa 240
atccatgcag agcagcacca acatttggtt acacagaact gtagtttgct cgaaggagtc 300
catctggctc tgtacttgac aaggcaagaa gagctatgta agtctgcagc ttctcaaaca 360
cag 363

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**SEQ ID NO: 10,554**

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atgatgaaac ctgcagccaa cactgccttc cacaagggtt tctggaaagg ctgaagctgg 180
agacggtaaa ccacaacacc gtcccaggtc actccaggtc accccagcta aagacattca 240
acaccagcca aaaggctaaa gtttagtttg aagggttcaa aggcaaatac actgaaaccc 300
acgtgtaaac ctgcctgggt ttcaaactgg aagagaaaca ctttggtgtc ttcaataacc 360
cagg 364

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**SEQ ID NO: 10,555**

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tgtgtgttgc tgctgccttc cgtgctgtct actgtatcct tcatgtgtct ccaaattggt 180
cacgccccat gggattacag aacacagcta cagaattagg atctcatggt aacaatgagg 240
aattaggtta ctgtagaact aaaatatggt taatgaaatt aaaatgcaat ggaaaaaaaa 300
tcaggcaaca gaacattctg atgaatttac aggactgatt atatcccacg gcactgaatg 360
acaaacagtt cttctccata cagtcgcaat tagaggcata gaagtcatac tgaatgctga 420
atagaagaac actgagaaga gcaggttata aatgaagggt ttcacattaa acagaaaaat 480
agacaaaatc atcggtaaga agctagctt 509

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**SEQ ID NO: 10,556**

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cagaagaaac ttattagaat aaggccacct aggaatgttc ttaacttttc cattcagctt 180
ttggctgata tatgaaaata caataaata catcctttcc ccaggtgcaa ggctaaacca 240
gcagctccaa gggcttggtc tacagtgtc agaaagacac actgccttaa aagtcaggct 300
agtgccctag ctccgggtggc ctctgcaaat gagg 334

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**SEQ ID NO: 10,557**

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tgggtctatat	tctcttttatt	gcatatactt	aatgtttcaa	aagaatgcag	attctgtgtt	480
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tttttt						546

**SEQ ID NO: 10,558**

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ttaatttggg	ccttactcat	ccagtagaag	atggaatttt	tgattctgga	aattttgagc	120
aattttctacg	ggagaagggt	aaagtcaatg	gcaaaactgg	aaatctcggg	aatgtttgtt	180
acattgaacg	cttcaagaat	aaaatcacag	ttgtttctga	gaaacagttc	tctaaaaggt	240
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tggttgcatc	tgacaaggag	acctacgaac	ttcgttactt	ccagattagt	caagatgaag	360
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aataaatgaa	gtatacatga	gaaataccaa	gaaattggct	tttagtttat	cagtgaataa	480
aaaatattat	actctcgaa					499

**SEQ ID NO: 10,559**

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tttagactat	tttactgagc	agactttata	aatgagatat	ctacaaggca	cttaaagtgt	120
tacagatgtt	ttaccttaag	aattatttaa	gttggtgttg	gttaagacag	ttttcagtgt	180
accgtaaatg	ttgtgttttc	agaaaaagac	aaaacgatgg	tgctgactgg	ttttctgtat	240
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tttttcactc	tccttagaat	tggaactatg	cagttaaggc	agataaaatg	tacagatgtt	360
tcatatatta	caggttacat	atataaatca	aaatttccta	tataaaactg	atttggggatt	420
tggggtggaa	atattttgaa	tattaattta	ttttt			455

**SEQ ID NO: 10,560**

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cagggagaaa	tccacactta	gggacttctt	tcttctcctg	cttatctgtt	tccatctcat	300
catccttggg	tggagggtct	gggatgggga	tgtccagtgg	ggccccgagg	gaagtcaagt	360
cagccacatt	gagggagtcc	tcttgcaaga	gctgattcag	gtatatgatt	ttctgtggca	420
agaatctgta	gaggaattcc	tcagcctcct	ggaaaagatt	ctgcctgaag	tcctcc	476

**SEQ ID NO: 10,561**

aaaatgcatt	ttcccttgtc	ctgtctttta	ctagatatatac	atgcttatat	ttatagtggg	60
tttcacagac	tataaaattg	aatgtatgaa	atttttattt	atatcagtgc	ttttaataat	120
gaagatattt	ttggagtaat	ggtgctgtct	tgtagcgagt	tattaatcat	agtaagattt	180
ttttctcttc	atttcttttt	tttgtttcat	attaacaatt	ttttttttac	acggacacaa	240
ccctctgaca	gtctttccaa	atattaaaat	catttgaata	tgtatgctgt	gatctgaaca	300
ctgctcaagc	catcaagcag	tcttcataca	gtttgcatta	taaaatctca	ttaaattctc	360
caagaaaaaa	taagttgaag	aattttattt	cctgaccatg	catccccctg	atttctgagt	420
ttcagttcag	attgtagatg	acaatataag	ctgccttccg	aaattgtcaa	catctgaatg	480

ttaagtccat tttcccatg gaagaagccc gtagttccat gaagtatgga ttaccatttg 540  
 tattttttcac taacagtaaa tgtatttttc ttattaattg tttgccttag gaatgatgaa 600  
 ttacattttt tgttccttct taccataaac atctgcattc ctcagctcag ccttccttgt 660  
 atgttgtttc tttataaatg gttgagctgc tgatgcaggt attcccaagc tancagtaca 720  
 aatcatttt 729

**SEQ ID NO: 10,562**

aaaatatttt aatcaggcag agttttatgg atagagaata gaagagaaaag gtagtaaata 60  
 ttgaacatat tccaatatag gaacctatct ctgttttagt acaaaatatt tctgacatct 120  
 gaactagagg tcaagagaat aaattcattt gtatacatct gagcaacctg tctttcagat 180  
 gataaagtat ctagcctttt ctgacaccat aatagttcat tttgtaggga ataagccatt 240  
 aggtgtatat aattgctttc tagaaatgac ctaatgtccc caaccacttt gtagtggcag 300  
 atcactgttt cacagcatat tttctcccaa ggaaagtatt caaaagagac tgcaactaac 360  
 annactctta tttcatcaaa attt 384

**SEQ ID NO: 10,563**

aaaagagcaa aatgtttatt ttttatatat cttcttagat gcctataaaa ctacaaagaa 60  
 aattacccta ttccactgaa aaggagagca gagaataaat taaacctttc tactatatgt 120  
 gccttttttt caactatgct aacttaatgc tgtacatgta atttcacttt tcagattaac 180  
 attgacagtt cgacaagaga gactatcatc aggaacattc aggaacccac tgaaacatgt 240  
 tttgaagaag ctcagaaaat agtctatatg catatggaaa gggattccta cccagattt 300  
 ctaaagtcag aaatgtacca aaaacttttg aaaactatgc agtccaacaa cagtttctga 360  
 ctacaactca aaagttt 377

**SEQ ID NO: 10,564**

aaaagtattt tctctacaga gaatcttatt agctatacaa aaatntgtac agtttttata 60  
 ctgaagctag tattgagctg cacttgaatt cacattctta gcaaaataat tgcttgagca 120  
 cacacacaca ttccacacgc atcattaaag gatagccatt tattcttcat cttcatcctc 180  
 ttctctctca tcttcatctt cttcttctc ctcctcctcc tcatcttctg gttcgttctt 240  
 cttctttgag cctgttgagg tgccagggcc cttctttcct gcttcacttt tgcccttggc 300  
 acgatatgca gcaatattct tttcatattt ctcttttagc ttagctgctt tctgttcata 360  
 tggntgttta tctttggctg actgctcaga ccacatttca cccaatttct ttgcagtatc 420  
 cccaatggat aggccagggt gttcactttt gatctttggg cgatgtt 467

**SEQ ID NO: 10,565**

aaagaacaga gttctggagt aaagaagcag gttccctttt cagtagacac ctcccgtctg 60  
 ctgttggaac acatcaattg tatcttcatt ctccatttcc aactgtgcag gtgtgtctgt 120  
 ttcattgatt gggtgcccgt caaatcggaa tntgatctgc ctcattgaca atccctgtcg 180  
 ttcacaatag gccttcatta gtttactaag tgggtgatgc ctcttaattc taaactgcac 240  
 cacagaacca tctgccccg ccacctcaa attaatatga tcgttgttct cagtcttgac 300  
 tctttccttg ggcttttctg cggccatggc gagcgccgga gtctcctcag 350

**SEQ ID NO: 10,566**

ctgaagctgc aggtgctgat cgagtcaaag agccctgaca tagccatgct ttttgaagaa 60  
 gccttttgtc acctgaaacc ccaggtttgt ctgccattgt ggatttcctg ggcagagtgg 120  
 agtgaaggtg ccaaaagcca agaagacact gaggcagtct ttaagaaagc tctcttagct 180  
 gtcataggtg ccgactcagt aaccctgaag aataagtacc tggattgggc ttatcgaagt 240  
 ggtggctaca aaaaggccag agctgtgttt 270

**SEQ ID NO: 10,567**

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ctgcctataa aactagactt ctgacgctgg gctccagctt cattctcaca ggtcatcatc 60
ctcatccggg agagcagttg tctgagcaac ctctaagtcg tgctcatact gtactgccaa 120
agctgggtcc atgacaactt ctgggtggggc gagagcaggc atggcaacaa attccaagtt 180
aggggtctcca atgagcttcc tagcaagcca gaggaagggc ttttcaaagt tgtagttact 240
tttggcagaa atgtcgtagt actgaagatt cttctttcgg tggaagacaa tggatttcgc 300
cttcactttc ctgtccttaa tatccacttt gttgccacac aacacaatgg ggatgttttc 360
acacactcgt accagatctc tatgccagtt aggcacattc ttgtaagtaa ctctcgatgt 420
tacatcaaac attatgatgg cacactgggc ttggatataa tagcc 465

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**SEQ ID NO: 10,568**

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ccttgatgat accattatcc tcattataga tgatgcacgg gcccctgcgc tggatacggc 60
gacggtttct cattttgcct ttgccagctc tcattcgctg agaggcatag acctacaaag 120
tgagcagttt tagtattctg attaagatag aatctctgca atagatcttc agagttttaa 180
ttccttttta cagatgatta aactgggcac aataacttgc caaggttaca cagagccata 240
aacagcagtt aggattcaaa cccaagtaat cgggctctga ggttcttggt ctctcacaca 300
ttaaggctta gctatactgc ccttatcttc tgaaattcaa agtgacaaac tgtgaacaag 360
gagtacaaa ctgtaaagt gctcattgaa cggacctttt tgatatcatt ccaggcttta 420
agtttcttaa ggagcaaaac agcttccttg gtcttcttgt agccttcaac tttatcttca 480
actaccaaag gaagttcagg aacttcctca atacgatgac ctttagacat gaccagtgt 540
ggtagggctg aggcagccag ggcagaacag atggcgtatc gtttttgggt tgtgttcact 600
cyacgatgcc aacggcgcca ggttttgggt ggtgcaaaca ttcggcctcc acgacacatg 660
tttccaaaag caccctgg 678

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**SEQ ID NO: 10,569**

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cgccaatctt cgctctgagg tgctgtctca ccggtgagac ctggaagcgg gcgagtctcg 60
tgctgtgtcg gacctgcagc ccctggcctt ccgccaccat ggagtacctc atcggtatcc 120
aaggccccga ctatgttctt gtgcgctccg accgggtggc cgccagcaat attgtccaga 180
tgaaggacga tcatgacaag atgtttaaga tgagtgaata gatattactc ctgtgtgttg 240
gagaggctgg agacactgta cagtttgtag aatatattca gaaaaacgtg caactttata 300
agatgcgaaa tggatatgaa ttgtctccca cggcagcagc taacttcaca cgccgaaacc 360
tggttgactg tcttcggagt cggaccccat atcatgtgaa cctcctctcg gctggctatg 420
atgagcatga agggccagcg ctgtattaca tggactacct ggcagccttg g 471

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**SEQ ID NO: 10,570**

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ccacatatgc ccctgtcatc tctgctgaga aagcctacca tgaacagctt actgtagcag 60
agatcaccaa tgcttgcttt gagccagcca accagatggg gaaatgtgac cctcgccatg 120
gtaaatacat ggcttgctgc ctgttatacc gtggtgacgt ggttcccaa gatgtcaatg 180
ctgccattgc caccatcaaa accaagcgta ccatccagtt tgtggattgg tgccccactg 240
gcttcaagg tggcattaat taccagctc cactgtggg gcctggcgga gacctggaaa 300
tgttcatgaa tgtttgaaag gaacaaaatt atcagggatg gctctttgcc atgggtctta 360
tttccacct cttttctgta agaaaaaaga acaatgtctt aatgtatttt t 411

```

**SEQ ID NO: 10,571**

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tttttttttc caagtaagcg tctatgcagg catcacaaac tttggcggat acagtagata 60
tgtatttctt tgatgctgaa aggtcagtc ctaagacaaa atcaaagtgc tcaaagaatt 120
aaaagcaaaa tgcatgtgc ttcttggaag aggtttccat ttgcaatgta atctgcattt 180
ctacaaatac tcaatgtcca aggcactag agggtgaaaa accaggcgag cgtcttccag 240
caggggtcag ggcagacca gagccaaaac tccatcctca gcccaacctt ggaggcccag 300
cag 303

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**SEQ ID NO: 10,572**

aaattgatct	ggtgttcctt	gcggggcttc	aattgcatct	aaataratgt	gagagttgaa	60
agacccataa	ggggcttctc	tcgctttacg	atgtcttatt	atTTTTTTTT	ccttcctctg	120
gttgatgaaa	tgccaggggtg	aaagggatag	ccaaataggc	taaagcaca	gtgccactct	180
agttattcsg	cagagtgtccc	aataaagggtc	cacgacaata	ccatcacaca	tccgctcggg	240
gatgaacaag	ggctgactga	ctgataagyt	cttgaaaatt	cttaagctca	ctgcatccct	300
tcaggtctcc	aaggaatgct	aagtctcctc	cctgccatga	gagacatgaa	atgaacttag	360
tgttggggaga	cggaagctgg	acggccctca	ggggctgacc	cgcagggact	ttgggatata	420
gcagagagag	cttggtcatga	cttattactc	caagctgtag	aaacctggaa	aatagctacc	480
ctgcagccca	tgcttggtca	actggaggac	caccttagtg	gaagggggac	aatcagggcc	540
tctggcctgc	catgtgcaca	agcataacaa	ttgcatttgt	tt		582

**SEQ ID NO: 10,573**

aaagaacaga	gttctggagt	aaagaagcag	gttccctttt	cagtagacac	ctcccgtctg	60
ctgttggaac	acatcaattg	tatcttcac	ctccatttcc	aactgtgcag	gtgtgtctgt	120
ttcattgatt	ggttgcccg	caaatcgga	tctgatctgc	ctcattgaca	atccctgtcg	180
ttcacaatag	gctttcatta	gtttactaag	tggtgtatgc	ctcttaatct	taaactgcac	240
cacagaacca	tcctgccccg	ccaccttcaa	attaatatga	tcgttgttct	cagtcttgac	300
tccttccttg	ggcttttctg	cggccatggc	gagcgccgg			339

**SEQ ID NO: 10,574**

aaatcaataa	gtaatctagg	actagcatta	tgtttgctag	acctggcatt	tgctcggtac	60
ataagggttca	aagtttcctt	tccttttttt	atTTTtttta	tattttgcaa	tgTTTTTTTT	120
ccataatatt	taagtttttc	gatgtttaga	tatttttctt	cgggtgaagca	caagtttctt	180
ttcatggtcc	ctgatcaatt	tt				202

**SEQ ID NO: 10,575**

ctgagaattc	gtccgctccc	gaggctgagc	agggcggggc	tgagtaaattg	ccggcttacc	60
atctctacca	tcattccggtt	tagtcatcca	acaagaagaa	atatgaaatt	ccagcaataa	120
gaaatgaaca	aaagattgga	gctgaagacc	taaagtgtct	gctttttgcc	cgttgaccag	180
ataaatagaa	ctatctgcat	tatctatgca	gcatgggggt	tttattattt	ttacctaaag	240
acgtctcttt	ttggtaataa	caaacgtgtt	ttttaaaaaa	gcttggtttt	tctcaataacg	300
ccttt						305

**SEQ ID NO: 10,576**

gagacaatgg	ccccgatgtt	atggagcccc	aaggcgtcat	cgagagtaac	tggaatgaga	60
ttgttgacag	ctttgatgac	atgaacctct	cggagtccct	tctccgtggc	atctacgcct	120
atggctttga	gaagccctct	gccatccags	agcgagccat	tctaccttgt	atcaaggggt	180
atgatgtgat	tgctcaagcc	caatctggga	ctgggaaaac	ggccacattt	g	231

**SEQ ID NO: 10,577**

cctgcagcat	gggaggtacc	acgctggcag	tcagcagtca	caccaggggtg	gtcagagaca	60
ctggtggcag	catctgtgct	tgcaactgca	ttcccagggt	gtctgttttg	ttcccaagtg	120
tctcccacaa	aattccccag	gaggttctcc	gattaaatgt	cctcaggggtg	aaaagcatgg	180
acaccaaate	actccgtatc	cacttccatg	agatgtcttg	atgctccagt	tcaatgagta	240
acaatttctc	aagaggctct	gattagtcca	ttaaaaata	agcaccacca	cctcattccc	300
cgtgatacag	cacatctagt	aatctaggcg	cctcagctaa	gctgcatagc	tcttagcaca	360
caggacaggt	cagcgttcac	acatcaacac	tataactatg	cggcggaact	agctccccgc	420
tagccgtcaa	ctactcagga	gactacctgt	gag			453

**SEQ ID NO: 10,578**

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aaaacggggg ggaacgggga aacgagctgt atctatgggt cacctcattc aacttccttg 60
agttatggca ctatgatgtt gcttaattag gtaagacatg gatatttgca ccgagtgcga 120
atactgttca taacaagggtc atagctagaa agacagatgg gctcaagtgt ggacaaataa 180
tgtcatcaag gtaatagatc aaaaatatta aagccctata aaagatctga gcagtcaact 240
ccaaaacatc cacatgacaa agtccttaaa atacaaatct cattactctt actcatgcaa 300
ctgctaaaaa atagtgtgca gatatgtatt tatatttgcc ttaaccttca aaatctaggg 360
acataaatct tgctttgtta aaaaaaata aaaaataaaa atagacagga atttgctaca 420
cttttccttc                                     430
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**SEQ ID NO: 10,579**

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ctgctgcccc tnagtnttct ttcctttctc ttttcttttc ctttcttctc tcttgtgcat 60
tcttcaggtc agtcatcaca ttcaaagtct tccataccca cataaccaca atgatcatgg 120
cattcaccag cagtgggggt gaaaatacta tagaaatgaa catccccctg gagtccgaaa 180
tactggtatt tcgaaaataa tctccagttc atcgagcccg cctcattgat gtattcagca 240
cagtagacta agatgactag acacagaaag ngccccgatc tgtacnctgt agctncggga 300
ggacaagcag gngaggagca cgcagagccg cgtggaaggg gg                                     342
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**SEQ ID NO: 10,580**

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tttttccgcc catgtagca ttgaagttgt gagctctact tgcttgtctt tatggccctt 60
taattcaagt aattggctcag tatccgtatg ggtcttttat accacccgct gggggctaaa 120
ctaatttagc tgctgctgta tacttactaa caaggaataa atgttaagct ttcttctcag 180
tattgatgga tggatcttaa aagtattttt atgtttcttt aacatggctt aaattttgaa 240
cttaatgtat caagttagta tggatcatatt aatacctgtg cttttcagat tcttcaaaca 300
cctaaatgaa agtgataaat tcaaaactga tccttttagt tcctcattat atgatatgaa 360
gggattaact gtagcaggat agtcaacctg accgtacggc atggtgcttt ttttcaggat 420
aaatcttcag acaaaaaagt gcaaacaaaa gggaaaaggg gagcaaaggg aaaacaggcc 480
gaagtggcta accaagaaac taaagaagac ttacctgcgg aaaacgggga aacgaagact 540
gaggagagtc cagcctctga tgaagcagga gagaaagaag ccaagtctga ttaataacca 600
tataccatgt cttatcagtg gtcctgtctt cccttcttgt acaatccaga nga                                     653
```

**Sequences with the same tissue expression profile as CD20 and CD52 and related sequences**

**SEQ ID NO: 10,581 - Lyl447 nucleotide sequence**

see, Figure 9

**SEQ ID NO: 10,582 - Lyl448 nucleotide sequence**

see, Figure 9

**SEQ ID NO: 10,583 - Lyl449 nucleotide sequence**

see, Figure 9

**SEQ ID NO: 10,584 - Lyl451 nucleotide sequence**

see, Figure 9

**SEQ ID NO: 10,585 - Lyl452 nucleotide sequence**

see, Figure 9

**SEQ ID NO: 10,586 - Lyl453 nucleotide sequence**



see, Figure 9

SEQ ID NO: 10,587 - Lyl454 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,588 - Lyl456 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,589 - Lyl458 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,590 - Lyl464 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,591 - Lyl480 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,592 - Lyl482 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,593 - Lyl483 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,594 - Lyl484 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,595 - Lyl485 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,596 - Lyl488 nucleotide sequence

see, Figure 9

SEQ ID NO: 10,597 - Lyl464 full length DNA sequence

see, Figure 10

SEQ ID NO: 10,598 - Lyl464 protein sequence

see, Figure 10

SEQ ID NOs: 10,599 - 10,819 - Lyl464 MHC Class binding peptides

see, Figure 12

SEQ ID NOs: 10,820- 10,842 - Lyl464 Immunogenic portions

see, Figure 14

SEQ ID NO: 10,843 - Ly1464 - sense primer

see, Figure 15

SEQ ID NO: 10,844 - Ly1464 - anti-sense primer

see, Figure 15

SEQ ID NO: 10,845 - Ly1464 1080 bp sequence

see, Figure 16

SEQ ID NO: 10,846 - Ly1484 4141 bp sequence

see, Figure 17

SEQ ID NO: 10,847 - Ly1484 protein sequence (long)

see, Figure 17

SEQ ID NO: 10,848 - Ly1484 protein sequence (short)

see, Figure 17

SEQ ID NO: 10,849 - 10,908 - Ly1484 long MHC class I binding peptides

see, Figure 19

SEQ ID NO: 10,909 -10,968 Ly1484 short MHC class I binding peptides

see, Figure 20

SEQ ID NO: 10,969 - Ly1488 Protein Sequence

see, Figure 27

SEQ ID NO: 10,970- Ly1488 2401 bp DNA sequence

see, Figure 27

SEQ ID NO: 10,971 - Ly1456P sequence

```
ggtgtgcatt atgttggatg attgtaaatt ttcagtgcaa aatgtaccgt gtcctaaatt 60
taaagacatg aaaaatatcc caagatcata ctagatcata atagcaattc ctttaciaat 120
gaattatgga ggtaactgat ctctaacagt ttccttcatt ttgttttaat gcacaagggc 180
agaggatctg ctgacccttg gaaccagcgt gactaaccac gtgctataga cacttcattg 240
tgtgcacccc aggggaagtca aagcgctttg ctccctcact gtctgtgagt cctcagccat 300
tagtacccca cccccgctg ctccaaaact tgagttattt caaatgtttc tctactgttca 360
tctctccact gaccaccact cagaaagcct ggagagagtc ccaagatgcc acccaccttc 420
cccaatccct cgccacagat ctgtgtctat ctcacactct gtaagtgccg ctttgc 476
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SEQ ID NO: 10,972 - Alternative Ly1456P sequence

aaatttagga cacggtacat tttccactga aaatttaciaa tcatccaaca taatgcacac 60  
 caccctcaa aggtaacatt agctcatata caaaatcatg gaaaacctca caacatcctt 120  
 ggaaggtaga tattgttata tccttacaaa aatttaatac acccattaac attcctattt 180  
 caaatagctc aatcgatata aacacataag acagcccaca attgtgatac agnattaaga 240  
 agaaaactcag gccagccgag gtgcctcaag cctgtaacct caacactttg ggaggctgag 300  
 gcgggcagat cacctgagcc caggagttca ggaccagcct ggacaacatg gtgagacccc 360  
 gtctctacaa aaagtacaaa aattagctgg gtgtggtgac ccacgcctgt agtcccagct 420  
 agttgggagg ctaagacggg aggatggctn gttgcttgag cccaaggagg t 471

**SEQ ID NO: 10,973 - Ly1456P PCR subtraction library fragment**

aaaataagct atggtttttc cagtagccaa aatgatcctg caccanagct catanactga 60  
 gaacctganc atgcaaancc acagtctggg tgaagggatg tctgctttgt aaatgacctg 120  
 ctaattcttt gcaaccacac gtaatttggt ttctgtgaac ccacagaagc agggccacca 180  
 aaaagggcct tgtctgctag cctggagtat acatgantca ctggcggtgg gatcagtcac 240  
 tttttaggct gccccatttt cctaacatgt taaaatgtgt gttctcagtc ttttcaagag 300  
 aggaagaagc aaagcggcac ttacagagtg tgtgatanga cacagatctg tggcgaggga 360  
 ttggggaagg tgggtggca 379

**SEQ ID NO: 10,974 - Ly1451 240 bp sequence**

cctaagccgc ctaaggggct gcctcggctg tccatcagtt acctcgtttc ctgagcagag 60  
 taattgggtg agattgttca tggaggcatt gctggctctc tagtcctgga acctacagtt 120  
 ggtccaattc attatgcaa agggtcctgc taggaggttc ttgttccaag tattgagatt 180  
 cccgagagaa gtaggtcccc ttagatagaa gcagagtttc tcagaggtat ttagcagcag 240

**SEQ ID NO: 10,975 - primer for His-Ly1452P**

5' gtgtcacatctacagtcaggcaggattctcc 3'

**SEQ ID NO: 10,976- primer for His-Ly1452P**

5' gttatgtagcggccgcttatcatgttgctgcagag 3'

**SEQ ID NO: 10,977- primer for His- TCL1**

5' gccgagtgcccgacactcgggg 3'

**SEQ ID NO: 10,978 - primer for His-TCL1**

5' catttgaattcatcagtcacatctggcagcagc 3'